Modeling Butterfly Distributions Across Southeast Asia

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Background

The world is literally crawling with insects, butterflies being the best known due to being brightly colored and charismatic. They have long been important model organisms for many topics in biology, ecology and evolution. Geographic information about the biodiversity of butterfly species is vital for understanding these topics and the changes that occur within them. Unfortunately, this information is severely lacking in Southeastern Asia, primarily due to sampling difficulties. We employ ecological niche modelling to fill in some of the gaps in species range maps for ten butterfly species distributed across this region – *Catopsilia pomona*, *Danaus genutia, Danaus melanippus, Euploea mulciber, Euploea tulliolus, Graphium agamemnon, Graphium sarpedon, Hypolimnas bolina, Melanitis leda* and *Papilio polytes.*

Methods

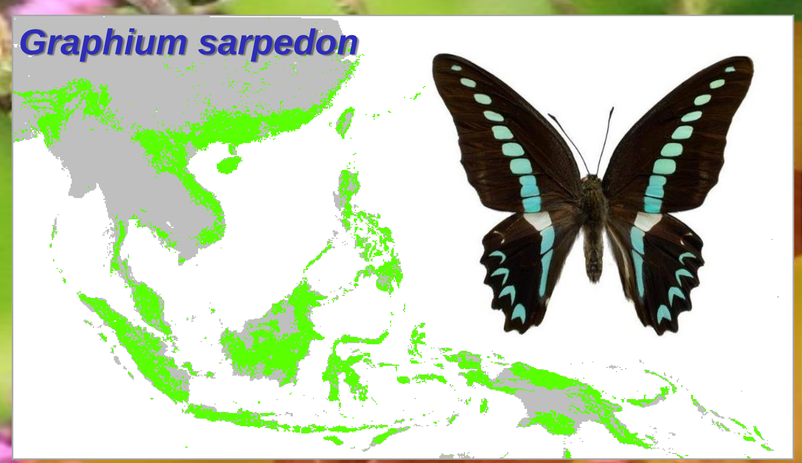
The MaxEnt software package was used to model species distributions. Species were chosen based on the number of occurrence points available on GBIF and from geolocated collection data in Southeast Asia. Model training regions encompassed East India, Southeast Asia and Oceania to reflect the dispersal ability of butterflies. Environmental variables were chosen based on biological relevance and downloaded from WorldClim (annual mean temperature, precipitation of the driest month, precipitation of the wettest month, maximum temperature of warmest month, minimum temperature of coldest month, altitude), SEDAC (2015 human density), and MODIS (vegetation index). MaxEnt was run with linear and hinge features to avoid overfit models due to a low number of occurrence points (n≈25), with ten crossvalidated replicates for testing model quality, and with the clamping feature to create more conservative models. Each model was thresholded at an appropriate value determined from omission/commission analysis and cropped to Southeast Asia. Results for three of the ten species are shown below.

Discussion

Ten butterfly species were modeled and projected onto Southeast Asia. Most of the distributions are extensive across the Philippines and Indonesia, emphasizing the extensive biodiversity and justification for conservation in these regions. Niche models like these can help characterize areas of potential collection sites, in turn providing more occurrence records and geographic information for future biodiversity analyses. Some data for this particular study may be biased however, as there is more locality information and thus more occurrence points for Australia and India than for Southeast Asia. Additional work to quantify this geographic bias could help in creating bias files for use in future modelling of this region.

Results

Graphium sarpedon



Hypolimnas bolina

Danaus melanippus

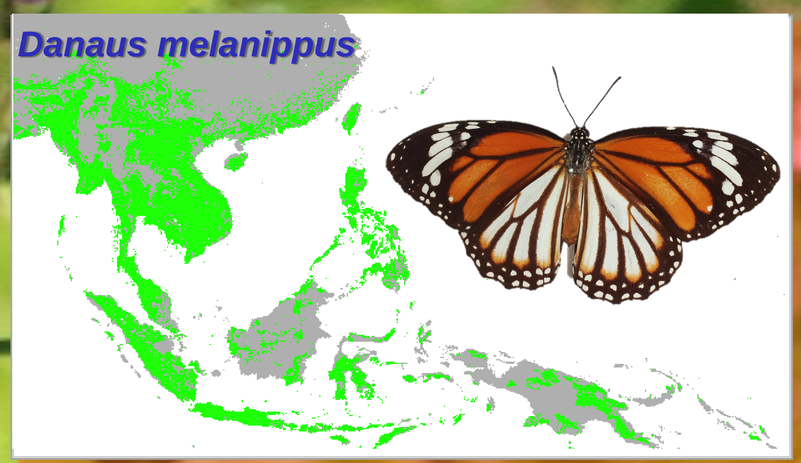


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Photo credit: http://biologyforhighschool.net, http://yutaka.it-n.jp, http://www.bubuleps.com, http://www.butterflycircle.com